

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:41:31 ; Search time 353 Seconds
(without alignments)
710.847 Million cell updates/sec

Title: US-09-883-839-1-C67_COPY_47_87
Perfect score: 41
Sequence: 1 tccctccgctgacgtcc.....ctctgtctcagccaggactg 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5662332 seqs, 3060109652 residues

Total number of hits satisfying chosen parameters: 11324664

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
	1	39.4	96.1	1431	14	US-10-080-917-6	Sequence 6, Appli
	2	39.4	96.1	1473	14	US-10-080-917-13	Sequence 13, Appl
	3	39.4	96.1	2149	14	US-10-080-917-12	Sequence 12, Appl
	4	39.4	96.1	2162	11	US-09-883-839-1	Sequence 1, Appli
	5	39.4	96.1	2162	11	US-09-883-839-3	Sequence 3, Appli
	6	39.4	96.1	2162	11	US-09-883-839-5	Sequence 5, Appli
	7	39.4	96.1	2162	11	US-09-883-839-7	Sequence 7, Appli
	8	39.4	96.1	2162	11	US-09-883-839-8	Sequence 8, Appli
	9	39.4	96.1	2162	15	US-10-225-567A-185	Sequence 185, App
	10	39.4	96.1	2162	17	US-10-305-720-1379	Sequence 1379, Ap
	11	39.4	96.1	2165	11	US-09-883-839-9	Sequence 9, Appli
	12	39.4	96.1	2279	19	US-10-477-714-33	Sequence 33, Appl
c	13	30.4	74.1	6494	15	US-10-311-455-1366	Sequence 1366, Ap
c	14	26.4	64.4	593	16	US-10-029-386-624	Sequence 624, App
c	15	25	61.0	1023	18	US-10-437-963-57733	Sequence 57733, A
	16	24.4	59.5	833	18	US-10-437-963-62219	Sequence 62219, A
	17	24.4	59.5	2319	18	US-10-437-963-62218	Sequence 62218, A
c	18	23.8	58.0	566	13	US-10-027-632-165648	Sequence 165648,
c	19	23.8	58.0	566	13	US-10-027-632-165649	Sequence 165649,
c	20	23.8	58.0	566	17	US-10-027-632-165648	Sequence 165648,
c	21	23.8	58.0	566	17	US-10-027-632-165649	Sequence 165649,
c	22	23.4	57.1	479	18	US-10-767-701-22509	Sequence 22509, A
	23	23.4	57.1	1618	10	US-09-841-720-1	Sequence 1, Appli
	24	23.4	57.1	1618	10	US-09-841-720-3	Sequence 3, Appli
c	25	22.8	55.6	304905	17	US-10-271-416-1	Sequence 1, Appli
c	26	22.6	55.1	40000	19	US-10-741-600-18013	Sequence 18013, A
	27	22.6	55.1	186391	13	US-10-087-192-136	Sequence 136, App
	28	22.4	54.6	722	18	US-10-767-701-7197	Sequence 7197, Ap
c	29	22	53.7	610	18	US-10-425-115-101365	Sequence 101365,
	30	22	53.7	32189	9	US-09-764-878-379	Sequence 379, App
	31	22	53.7	32189	14	US-10-079-854-379	Sequence 379, App
	32	22	53.7	32221	9	US-09-764-878-377	Sequence 377, App
	33	22	53.7	32221	14	US-10-079-854-377	Sequence 377, App
	34	22	53.7	149671	17	US-10-236-031B-53	Sequence 53, Appl
	35	21.8	53.2	494	13	US-10-027-632-303342	Sequence 303342,
	36	21.8	53.2	494	17	US-10-027-632-303342	Sequence 303342,
	37	21.8	53.2	503	13	US-10-027-632-87081	Sequence 87081, A
	38	21.8	53.2	503	17	US-10-027-632-87081	Sequence 87081, A
	39	21.8	53.2	2116	17	US-10-424-599-89323	Sequence 89323, A
c	40	21.8	53.2	13784	18	US-10-719-993-6793	Sequence 6793, Ap
	41	21.8	53.2	15922	18	US-10-741-601-5643	Sequence 5643, Ap
	42	21.8	53.2	15922	18	US-10-719-993-6795	Sequence 6795, Ap
	43	21.8	53.2	15922	19	US-10-741-600-17648	Sequence 17648, A
	44	21.8	53.2	23909	13	US-10-087-192-604	Sequence 604, App
c	45	21.8	53.2	28553	18	US-10-741-601-5763	Sequence 5763, Ap

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OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:08:06 ; Search time 570 Seconds
(without alignments)
3485.375 Million cell updates/sec

Title: US-09-883-839-1-C67_COPY_47_87
Perfect score: 41
Sequence: 1 tccctccgcctgacgctcc.....ctctgtctcagccaggactg 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	39.4	96.1	1473	9	HSU12569	U12569 Human mu op
2	39.4	96.1	1610	6	AR106017	AR106017 Sequence
3	39.4	96.1	1610	9	HUMOPIOIDA	L29301 Homo sapien

	4	39.4	96.1	2150	6	CQ725069	CQ725069 Sequence
	5	39.4	96.1	2160	6	AR162044	AR162044 Sequence
	6	39.4	96.1	2162	6	A87781	A87781 Sequence 7
	7	39.4	96.1	2162	6	AR181331	AR181331 Sequence
	8	39.4	96.1	2162	6	AR182295	AR182295 Sequence
	9	39.4	96.1	2162	6	AR270816	AR270816 Sequence
	10	39.4	96.1	2162	6	AR301230	AR301230 Sequence
	11	39.4	96.1	2162	6	AX548900	AX548900 Sequence
	12	39.4	96.1	2162	9	HUMMOR1X	L25119 Human Mu op
	13	39.4	96.1	3759	9	AF153500	AF153500 Homo sapi
	14	39.4	96.1	83889	9	AY587764	AY587764 Homo sapi
c	15	39.4	96.1	96310	9	AL136444	AL136444 Human DNA
	16	39.4	96.1	182048	2	AC027439	AC027439 Homo sapi
c	17	39.4	96.1	182383	2	AC021745	AC021745 Homo sapi
c	18	30.4	74.1	6494	6	AX346295	AX346295 Sequence
c	19	30.4	74.1	6494	6	AX348524	AX348524 Sequence
	20	26.2	63.9	1881	4	AF521309	AF521309 Sus scrofa
	21	26.2	63.9	1881	4	PIGMUOPR	L38645 Sus scrofa
c	22	25.6	62.4	2522	6	CQ726580	CQ726580 Sequence
c	23	25.6	62.4	4059	9	AY341075	AY341075 Homo sapi
c	24	25.6	62.4	4113	6	CQ850147	CQ850147 Sequence
c	25	25.6	62.4	4113	9	AK127248	AK127248 Homo sapi
c	26	25.6	62.4	4152	6	CQ850141	CQ850141 Sequence
c	27	25.6	62.4	4152	9	AK127241	AK127241 Homo sapi
c	28	25.6	62.4	5281	9	AB070620	AB070620 Homo sapi
c	29	25.6	62.4	7327	9	AB075865	AB075865 Homo sapi
	30	25.6	62.4	122394	9	AC011364	AC011364 Homo sapi
	31	25.2	61.5	189049	9	AC008667	AC008667 Homo sapi
	32	25.2	61.5	244928	2	AC097177	AC097177 Rattus no
c	33	25.2	61.5	245125	2	AC133759	AC133759 Rattus no
c	34	25.2	61.5	247269	2	AC120819	AC120819 Rattus no
c	35	25	61.0	868	8	AK061899	AK061899 Oryza sat
	36	25	61.0	73666	9	HSJ333B15	AL109954 Human DNA
c	37	25	61.0	88854	8	AP005607	AP005607 Oryza sat
	38	25	61.0	245452	2	AC094820	AC094820 Rattus no
c	39	25	61.0	255725	2	AC134804	AC134804 Rattus no
	40	24.6	60.0	110000	2	AP006496_6	Continuation (7 of
	41	24.6	60.0	241726	2	AC097121	AC097121 Rattus no
	42	24.4	59.5	776	8	AK120302	AK120302 Oryza sat
	43	24.4	59.5	120832	9	AP001068	AP001068 Homo sapi
	44	24.4	59.5	146350	9	HS225L15	AL773604 Homo sapi
	45	24.4	59.5	161001	8	AP005111	AP005111 Oryza sat

Run on: May 14, 2005, 05:08:06 ; Search time 280 Seconds
 (without alignments)
 866.819 Million cell updates/sec

Title: US-09-883-839-1-C67_COPY_47_87
 Perfect score: 41
 Sequence: 1 tccctccgcctgacgctcc.....ctctgtctcagccaggactg 41

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	39.4	96.1	1431	6	ABS54812	Abs54812 cDNA enco
2	39.4	96.1	1473	6	ABS54816	Abs54816 cDNA enco
3	39.4	96.1	1610	2	AAQ89226	Aaq89226 Human mu
4	39.4	96.1	1610	3	AAA59503	Aaa59503 cDNA enco
5	39.4	96.1	1610	13	ADR44881	Adr44881 Human mu-
6	39.4	96.1	2149	6	ABS54815	Abs54815 cDNA enco
7	39.4	96.1	2160	2	AAQ93102	Aaq93102 Human mu
8	39.4	96.1	2162	2	AAV61995	Aav61995 Human mu-
9	39.4	96.1	2162	2	AAV61991	Aav61991 Human mu-
10	39.4	96.1	2162	2	AAV61988	Aav61988 Human mu-
11	39.4	96.1	2162	2	AAV61984	Aav61984 Human mu-

12	39.4	96.1	2162	2	AAV61994	Aav61994 Human mu-
13	39.4	96.1	2162	2	AAV61987	Aav61987 Human mu-
14	39.4	96.1	2162	2	AAV61992	Aav61992 Human mu-
15	39.4	96.1	2162	2	AAV61990	Aav61990 Human mu-
16	39.4	96.1	2162	2	AAV61993	Aav61993 Human mu-
17	39.4	96.1	2162	2	AAV61985	Aav61985 Human mu-
18	39.4	96.1	2162	2	AAV61989	Aav61989 Human mu-
19	39.4	96.1	2162	3	AAZ88470	Aaz88470 Human mu
20	39.4	96.1	2162	6	ABK14953	Abk14953 Human mu
21	39.4	96.1	2162	8	ABZ42697	Abz42697 Human opi
22	39.4	96.1	2162	10	ADC21534	Adc21534 Human DNA
23	39.4	96.1	2162	10	ACA56781	Aca56781 Human sig
24	39.4	96.1	2162	12	ADI56577	Adi56577 Human pol
25	39.4	96.1	2162	12	ADO30013	Ado30013 Human GPC
26	39.4	96.1	2279	8	AAD51226	Aad51226 Human REM
27	39.4	96.1	9426	13	ADR44835	Adr44835 FIV opioi
c 28	39.4	96.1	9569	13	ADR44842	Adr44842 FIV-NSE-H
29	39.4	96.1	10472	13	ADR44876	Adr44876 Plasmid p
30	37.8	92.2	2162	2	AAV61986	Aav61986 Human mu-
c 31	30.4	74.1	6494	6	ABL33393	Abl33393 Human imm
c 32	30.4	74.1	6494	6	AAD28391	Aad28391 Human che
c 33	26.4	64.4	593	12	ACH67429	Ach67429 Human gen
34	26.2	63.9	1881	13	ADR44850	Adr44850 Porcine m
c 35	25.6	62.4	3990	5	AAS80853	Aas80853 DNA encod
c 36	25.6	62.4	3990	10	ADC32436	Adc32436 Human nov
c 37	25.6	62.4	4113	13	ADR07110	Adr07110 Full leng
c 38	25.6	62.4	4152	13	ADR07104	Adr07104 Full leng
39	23.4	57.1	1415	13	ADR44844	Adr44844 Bovine mu
40	23.4	57.1	1618	2	AAQ89222	Aaq89222 Rat mu op
41	23.4	57.1	1618	2	AAQ89223	Aaq89223 Transcrip
42	23.4	57.1	1618	3	AAA59499	Aaa59499 cDNA enco
c 43	23	56.1	2467	4	ABL09033	Abl09033 Drosophil
c 44	23	56.1	11508	4	ABL09032	Abl09032 Drosophil
c 45	22.8	55.6	304905	11	ADP75180	Adp75180 Human End

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OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:08:06 ; Search time 82.4 Seconds
(without alignments)
814.167 Million cell updates/sec

Title: US-09-883-839-1-C67_COPY_47_87
Perfect score: 41
Sequence: 1 tccctccgcctgacgtcc.....ctctgtctcagccaggactg 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	39.4	96.1	1610	3	US-08-889-108-7	Sequence 7, Appli
2	39.4	96.1	1610	5	PCT-US94-10358-7	Sequence 7, Appli
3	39.4	96.1	2160	3	US-08-188-275A-1	Sequence 1, Appli
4	39.4	96.1	2162	3	US-09-351-198-1	Sequence 1, Appli
5	39.4	96.1	2162	3	US-09-113-426-1	Sequence 1, Appli
6	39.4	96.1	2162	4	US-09-016-434-1379	Sequence 1379, Ap
7	39.4	96.1	2162	4	US-09-355-709C-7	Sequence 7, Appli
8	23.8	58.0	97989	4	US-09-949-016-13208	Sequence 13208, A
9	23.4	57.1	1618	3	US-08-889-108-1	Sequence 1, Appli
10	23.4	57.1	1618	3	US-08-889-108-3	Sequence 3, Appli
11	23.4	57.1	1618	3	US-08-120-601B-1	Sequence 1, Appli

	12	23.4	57.1	1618	3	US-08-120-601B-3	Sequence 3, Appli
	13	23.4	57.1	1618	5	PCT-US94-10358-1	Sequence 1, Appli
	14	23.4	57.1	1618	5	PCT-US94-10358-3	Sequence 3, Appli
c	15	23	56.1	601	4	US-09-949-016-109347	Sequence 109347,
	16	23	56.1	979	4	US-09-270-767-565	Sequence 565, App
	17	23	56.1	979	4	US-09-270-767-15847	Sequence 15847, A
	18	23	56.1	154600	4	US-09-949-016-14757	Sequence 14757, A
	19	22.6	55.1	10029	4	US-09-949-016-11846	Sequence 11846, A
	20	22.6	55.1	10029	4	US-09-949-016-16140	Sequence 16140, A
	21	22.6	55.1	31199	4	US-09-949-016-16516	Sequence 16516, A
	22	22.2	54.1	55328	4	US-09-949-016-12747	Sequence 12747, A
	23	22.2	54.1	55330	4	US-09-949-016-17146	Sequence 17146, A
c	24	21.8	53.2	601	4	US-09-949-016-177112	Sequence 177112,
	25	21.8	53.2	7853	4	US-09-949-016-12034	Sequence 12034, A
	26	21.8	53.2	7853	4	US-09-949-016-14225	Sequence 14225, A
	27	21.8	53.2	92344	4	US-09-949-016-16802	Sequence 16802, A
	28	21.6	52.7	335	4	US-09-621-976-13385	Sequence 13385, A
	29	21.6	52.7	66933	4	US-09-544-398B-11	Sequence 11, Appl
	30	21.6	52.7	66933	4	US-09-543-771B-11	Sequence 11, Appl
	31	21.6	52.7	72049	4	US-09-544-398B-9	Sequence 9, Appli
	32	21.6	52.7	72049	4	US-09-543-771B-9	Sequence 9, Appli
	33	21.6	52.7	140844	4	US-09-949-016-14199	Sequence 14199, A
c	34	21.4	52.2	3881	3	US-09-042-353-369	Sequence 369, App
c	35	21.4	52.2	3881	3	US-08-758-417A-217	Sequence 217, App
c	36	21.4	52.2	13999	3	US-08-444-644-24	Sequence 24, Appl
c	37	21.4	52.2	13999	3	US-08-232-246A-24	Sequence 24, Appl
c	38	21.4	52.2	72455	4	US-09-949-016-13793	Sequence 13793, A
c	39	21.4	52.2	104475	4	US-09-949-016-12115	Sequence 12115, A
c	40	21.4	52.2	111282	3	US-09-754-250-3	Sequence 3, Appli
c	41	21.2	51.7	42610	4	US-09-949-016-13882	Sequence 13882, A
c	42	21	51.2	601	4	US-09-949-016-205678	Sequence 205678,
c	43	21	51.2	601	4	US-09-949-016-205679	Sequence 205679,
c	44	21	51.2	601	4	US-09-949-016-205680	Sequence 205680,
c	45	21	51.2	601	4	US-09-949-016-205681	Sequence 205681,

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:08:06 ; Search time 2468.2 Seconds
(without alignments)
632.297 Million cell updates/sec

Title: US-09-883-839-1-C67_COPY_47_87
Perfect score: 41
Sequence: 1 tcccctccgcctgacgctcc.....ctctgtctcagccaggactg 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	39.4	96.1	582	5	BP346782	BP346782 BP346782
c	2	25.6	62.4	546	2	BE302852	BE302852 ba70a03.y
c	3	25.6	62.4	601	2	BF026883	BF026883 601670928
c	4	25.6	62.4	602	5	BX474301	BX474301 DKFZp6860
c	5	25.6	62.4	627	2	BE302610	BE302610 ba73a06.y
	6	25.4	62.0	234	9	CL567180	CL567180 OB__Ba003
	7	25.4	62.0	306	9	CL580031	CL580031 OB__Ba003
	8	25.4	62.0	485	9	CL600049	CL600049 OB__Ba006
c	9	25	61.0	221	8	BZ886648	BZ886648 CH240_284

c	10	25	61.0	243	1	AA750503	AA750503 ISGS0079
c	11	25	61.0	244	1	AU068620	AU068620 AU068620
c	12	25	61.0	328	6	C74287	C74287 C74287 Rice
c	13	25	61.0	430	6	C74012	C74012 C74012 Rice
c	14	25	61.0	450	7	D49185	D49185 RICS15893A
c	15	25	61.0	460	6	C73380	C73380 C73380 Rice
c	16	25	61.0	468	1	AU162741	AU162741 AU162741
c	17	25	61.0	511	7	CF292624	CF292624 30DGS--01
c	18	25	61.0	515	7	CF315785	CF315785 HD--04-N0
c	19	25	61.0	524	7	CF291922	CF291922 14ROOT--0
c	20	25	61.0	538	7	CF335117	CF335117 JMT--04-K
c	21	25	61.0	546	7	CF332626	CF332626 JMT--01-D
c	22	25	61.0	552	7	CF335003	CF335003 JMT--04-I
c	23	25	61.0	556	7	CF291247	CF291247 14ROOT--0
c	24	25	61.0	570	7	CF291013	CF291013 14ROOT--0
c	25	25	61.0	577	7	CF310992	CF310992 ABF--05-P
c	26	25	61.0	584	7	CF308926	CF308926 ABF--02-O
c	27	25	61.0	630	7	CF316819	CF316819 HD--06-E1
c	28	25	61.0	633	7	CF333746	CF333746 JMT--02-M
c	29	25	61.0	655	7	CF291820	CF291820 14ROOT--0
c	30	25	61.0	716	7	CF281557	CF281557 14ETL--08
	31	24.8	60.5	182	7	CF572653	CF572653 MCSA052C0
c	32	24.8	60.5	339	4	BG463857	BG463857 EM1_51_G0
	33	24.8	60.5	1015	9	AG099856	AG099856 Pan trogl
	34	24.4	59.5	663	9	CL721051	CL721051 OR_BBa004
	35	24.4	59.5	692	9	AG151883	AG151883 Pan trogl
c	36	24.2	59.0	215	5	BP732360	BP732360 BP732360
	37	24.2	59.0	346	5	BP699442	BP699442 BP699442
c	38	24	58.5	52	7	CF281204	CF281204 14ETL--08
c	39	24	58.5	649	6	CA246735	CA246735 SCSGFL5C0
c	40	24	58.5	711	6	CA155353	CA155353 SCACRZ310
c	41	24	58.5	785	6	CA239394	CA239394 SCRFFL503
	42	23.8	58.0	246	9	CL574873	CL574873 OB__Ba002
	43	23.8	58.0	304	9	CL547245	CL547245 OB__Ba008
	44	23.8	58.0	515	9	CL541343	CL541343 OB__Ba006
	45	23.8	58.0	549	6	CB850738	CB850738 UI-CF-EN1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:08:06 ; Search time 570 Seconds
(without alignments)
3485.375 Million cell updates/sec

Title: US-09-883-839-1-A174_COPY_154_194
Perfect score: 41
Sequence: 1 gaaaagtctcggtgctcctg.....ctacctcgcacagcggtgcc 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	39.4	96.1	158	9	AY292291	AY292291 Homo sapi
2	39.4	96.1	163	9	AY292290	AY292290 Homo sapi
3	39.4	96.1	1468	9	AY364230	AY364230 Homo sapi

	4	39.4	96.1	1473	9	HSU12569	U12569 Human mu op
	5	39.4	96.1	2150	6	CQ725069	CQ725069 Sequence
	6	39.4	96.1	2160	6	AR162044	AR162044 Sequence
	7	39.4	96.1	2162	6	A87781	A87781 Sequence 7
	8	39.4	96.1	2162	6	AR181331	AR181331 Sequence
	9	39.4	96.1	2162	6	AR182295	AR182295 Sequence
	10	39.4	96.1	2162	6	AR270816	AR270816 Sequence
	11	39.4	96.1	2162	6	AR301230	AR301230 Sequence
	12	39.4	96.1	2162	6	AX548900	AX548900 Sequence
	13	39.4	96.1	2162	9	HUMMOR1X	L25119 Human Mu op
	14	39.4	96.1	3759	9	AF153500	AF153500 Homo sapi
	15	39.4	96.1	83889	9	AY587764	AY587764 Homo sapi
c	16	39.4	96.1	96310	9	AL136444	AL136444 Human DNA
	17	39.4	96.1	182048	2	AC027439	AC027439 Homo sapi
c	18	39.4	96.1	182383	2	AC021745	AC021745 Homo sapi
	19	36.2	88.3	1399	9	AY038989	AY038989 Macaca fa
	20	34.6	84.4	1610	6	AR106017	AR106017 Sequence
	21	34.6	84.4	1610	9	HUMOPIOIDA	L29301 Homo sapien
c	22	30.4	74.1	520	11	G53082	G53082 SHGC-84785
c	23	29.8	72.7	6494	6	AX346295	AX346295 Sequence
c	24	29.8	72.7	6494	6	AX348524	AX348524 Sequence
	25	25.6	62.4	1388	9	AY036623	AY036623 Homo sapi
	26	25.6	62.4	1464	9	AY036622	AY036622 Homo sapi
	27	25.4	62.0	1293	9	BC074927	BC074927 Homo sapi
	28	24.4	59.5	77521	5	BX927398	BX927398 Zebrafish
	29	24.4	59.5	221392	5	BX571958	BX571958 Zebrafish
	30	23.6	57.6	50	6	CQ004363	CQ004363 Sequence
	31	23.6	57.6	3592	9	BC045640	BC045640 Homo sapi
	32	23.6	57.6	185412	2	AC103636	AC103636 Mus muscu
	33	23.6	57.6	201951	2	AC102766	AC102766 Mus muscu
	34	23	56.1	6494	6	AX346294	AX346294 Sequence
	35	23	56.1	6494	6	AX348523	AX348523 Sequence
	36	23	56.1	79960	2	AC135195	AC135195 Rattus no
c	37	22.6	55.1	65140	6	AX211705	AX211705 Sequence
c	38	22.6	55.1	123580	1	AF263912	AF263912 Streptomy
c	39	22.6	55.1	125401	6	AX211739	AX211739 Sequence
	40	22.6	55.1	226555	2	AC134913	AC134913 Mus muscu
c	41	22.6	55.1	254766	2	AC127117	AC127117 Rattus no
	42	22.6	55.1	257210	2	AC098622	AC098622 Rattus no
c	43	22.6	55.1	326891	2	AC129744	AC129744 Rattus no
	44	22.4	54.6	206709	10	AL772319	AL772319 Mouse DNA
	45	22.2	54.1	238	9	HS71E7R	Z55900 H.sapiens C

OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:08:06 ; Search time 280 Seconds
(without alignments)
866.819 Million cell updates/sec

Title: US-09-883-839-1-A174_COPY_154_194
Perfect score: 41
Sequence: 1 gaaaagtctcgggtgctcctg.....ctacctcgcacagcggtgcc 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				ID	Description
	No.	Score	Match	Length	DB			
c	1	39.4	96.1	593	12	ACH67429	Ach67429 Human gen	
	2	39.4	96.1	1431	6	ABS54812	Abs54812 cDNA enco	
	3	39.4	96.1	1473	6	ABS54816	Abs54816 cDNA enco	
	4	39.4	96.1	2149	6	ABS54815	Abs54815 cDNA enco	
	5	39.4	96.1	2160	2	AAQ93102	Aaq93102 Human mu	
	6	39.4	96.1	2162	2	AAV61995	Aav61995 Human mu-	
	7	39.4	96.1	2162	2	AAV61986	Aav61986 Human mu-	
	8	39.4	96.1	2162	2	AAV61991	Aav61991 Human mu-	
	9	39.4	96.1	2162	2	AAV61984	Aav61984 Human mu-	

	10	39.4	96.1	2162	2	AAV61994	Aav61994 Human mu-
	11	39.4	96.1	2162	2	AAV61987	Aav61987 Human mu-
	12	39.4	96.1	2162	2	AAV61992	Aav61992 Human mu-
	13	39.4	96.1	2162	2	AAV61990	Aav61990 Human mu-
	14	39.4	96.1	2162	2	AAV61993	Aav61993 Human mu-
	15	39.4	96.1	2162	2	AAV61985	Aav61985 Human mu-
	16	39.4	96.1	2162	2	AAV61989	Aav61989 Human mu-
	17	39.4	96.1	2162	3	AAZ88470	Aaz88470 Human mu
	18	39.4	96.1	2162	6	ABK14953	Abk14953 Human mu
	19	39.4	96.1	2162	8	ABZ42697	Abz42697 Human opi
	20	39.4	96.1	2162	10	ADC21534	Adc21534 Human DNA
	21	39.4	96.1	2162	10	ACA56781	Aca56781 Human sig
	22	39.4	96.1	2162	12	ADI56577	Adi56577 Human pol
	23	39.4	96.1	2162	12	ADO30013	Ado30013 Human GPC
	24	39.4	96.1	2279	8	AAD51226	Aad51226 Human REM
	25	39.4	96.1	9426	13	ADR44835	Adr44835 FIV opioi
c	26	39.4	96.1	9569	13	ADR44842	Adr44842 FIV-NSE-H
	27	39.4	96.1	10472	13	ADR44876	Adr44876 Plasmid p
	28	37.8	92.2	2162	2	AAV61988	Aav61988 Human mu-
	29	34.6	84.4	1610	2	AAQ89226	Aaq89226 Human mu
	30	34.6	84.4	1610	3	AAA59503	Aaa59503 cDNA enco
	31	34.6	84.4	1610	13	ADR44881	Adr44881 Human mu-
c	32	29.8	72.7	6494	6	ABL33393	Abl33393 Human imm
c	33	29.8	72.7	6494	6	AAD28391	Aad28391 Human che
	34	25.6	62.4	1388	10	ADG42251	Adg42251 Mu-opioid
	35	25.6	62.4	1464	10	ADG42250	Adg42250 Mu-opioid
	36	23.6	57.6	50	4	AAL29795	Aal29795 Human SNP
	37	23	56.1	6494	6	ABL33392	Abl33392 Human imm
	38	23	56.1	6494	6	AAD28390	Aad28390 Human che
c	39	22.6	55.1	65140	4	AAD17184	Aad17184 Streptomy
c	40	22.6	55.1	125401	4	AAD17186	Aad17186 Streptomy
	41	22	53.7	468	9	ACH37173	Ach37173 Human end
c	42	22	53.7	567	4	AAS57406	Aas57406 cDNA #82
	43	22	53.7	932	8	ACA57069	Aca57069 Human adi
	44	22	53.7	3294	9	AAL61264	Aal61264 Human kar
	45	22	53.7	3294	13	ACN39649	Acn39649 Tumour-as

OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:08:06 ; Search time 82.4 Seconds
(without alignments)
814.167 Million cell updates/sec

Title: US-09-883-839-1-A174_COPY_154_194
Perfect score: 41
Sequence: 1 gaaaagtctcggtgctcctg.....ctacctcgcacagcggtgcc 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	39.4	96.1	2160	3	US-08-188-275A-1	Sequence 1, Appli
2	39.4	96.1	2162	3	US-09-351-198-1	Sequence 1, Appli
3	39.4	96.1	2162	3	US-09-113-426-1	Sequence 1, Appli
4	39.4	96.1	2162	4	US-09-016-434-1379	Sequence 1379, Ap
5	39.4	96.1	2162	4	US-09-355-709C-7	Sequence 7, Appli
6	34.6	84.4	1610	3	US-08-889-108-7	Sequence 7, Appli
7	34.6	84.4	1610	5	PCT-US94-10358-7	Sequence 7, Appli
8	22	53.7	5907	4	US-09-976-594-892	Sequence 892, App
9	21.8	53.2	325034	4	US-09-949-016-14957	Sequence 14957, A
10	21.8	53.2	389504	4	US-09-949-016-11774	Sequence 11774, A
11	21.6	52.7	1408	4	US-09-205-258-31	Sequence 31, Appl
12	21.2	51.7	1000	3	US-09-641-638-631	Sequence 631, App

	13	21.2	51.7	1000	4	US-10-170-097-631	Sequence 631, App
	14	21.2	51.7	2343	3	US-09-641-638-652	Sequence 652, App
	15	21.2	51.7	2343	4	US-10-170-097-652	Sequence 652, App
	16	21.2	51.7	20674	3	US-09-641-638-651	Sequence 651, App
	17	21.2	51.7	20674	4	US-10-170-097-651	Sequence 651, App
c	18	20.6	50.2	1761	4	US-09-252-991A-14440	Sequence 14440, A
c	19	20.4	49.8	5132	4	US-09-902-540-597	Sequence 597, App
c	20	20.4	49.8	7553	4	US-09-902-540-920	Sequence 920, App
	21	20.4	49.8	15572	4	US-09-902-540-1131	Sequence 1131, Ap
c	22	20.2	49.3	64309	4	US-09-949-016-14581	Sequence 14581, A
c	23	20	48.8	5418	4	US-09-902-540-675	Sequence 675, App
c	24	20	48.8	60304	4	US-09-949-016-11995	Sequence 11995, A
c	25	20	48.8	60304	4	US-09-949-016-17264	Sequence 17264, A
	26	19.8	48.3	1254	4	US-09-774-528-70	Sequence 70, Appl
c	27	19.8	48.3	62072	4	US-09-949-016-16076	Sequence 16076, A
	28	19.6	47.8	601	4	US-09-949-016-29288	Sequence 29288, A
	29	19.6	47.8	601	4	US-09-949-016-40393	Sequence 40393, A
	30	19.6	47.8	601	4	US-09-949-016-46813	Sequence 46813, A
	31	19.6	47.8	601	4	US-09-949-016-46826	Sequence 46826, A
	32	19.6	47.8	601	4	US-09-949-016-111464	Sequence 111464,
	33	19.6	47.8	601	4	US-09-949-016-111477	Sequence 111477,
c	34	19.6	47.8	16672	4	US-09-949-016-12322	Sequence 12322, A
c	35	19.6	47.8	16672	4	US-09-949-016-12880	Sequence 12880, A
c	36	19.6	47.8	16672	4	US-09-949-016-13104	Sequence 13104, A
c	37	19.6	47.8	16672	4	US-09-949-016-13105	Sequence 13105, A
c	38	19.6	47.8	16672	4	US-09-949-016-14818	Sequence 14818, A
c	39	19.6	47.8	16672	4	US-09-949-016-14819	Sequence 14819, A
	40	19.4	47.3	601	4	US-09-949-016-66776	Sequence 66776, A
	41	19.4	47.3	46253	4	US-09-949-016-11890	Sequence 11890, A
	42	19.4	47.3	46257	4	US-09-949-016-13711	Sequence 13711, A
	43	19.4	47.3	138282	4	US-09-949-016-15307	Sequence 15307, A
	44	19.4	47.3	229354	4	US-09-705-400-64	Sequence 64, Appl
	45	19.2	46.8	659	4	US-08-857-636-59	Sequence 59, Appl

OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:41:31 ; Search time 353 Seconds
(without alignments)
710.847 Million cell updates/sec

Title: US-09-883-839-1-A174_COPY_154_194
Perfect score: 41
Sequence: 1 gaaaagtctcggtgctcctg.....ctacctcgcacagcggtgcc 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5662332 seqs, 3060109652 residues

Total number of hits satisfying chosen parameters: 11324664

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match Length	DB	ID	Description
No.					

c	1	39.4	96.1	593	16	US-10-029-386-624	Sequence 624, App
	2	39.4	96.1	1431	14	US-10-080-917-6	Sequence 6, Appli
	3	39.4	96.1	1473	14	US-10-080-917-13	Sequence 13, Appl
	4	39.4	96.1	2149	14	US-10-080-917-12	Sequence 12, Appl
	5	39.4	96.1	2162	11	US-09-883-839-1	Sequence 1, Appli
	6	39.4	96.1	2162	11	US-09-883-839-3	Sequence 3, Appli
	7	39.4	96.1	2162	11	US-09-883-839-5	Sequence 5, Appli
	8	39.4	96.1	2162	11	US-09-883-839-7	Sequence 7, Appli
	9	39.4	96.1	2162	11	US-09-883-839-8	Sequence 8, Appli
	10	39.4	96.1	2162	15	US-10-225-567A-185	Sequence 185, App
	11	39.4	96.1	2162	17	US-10-305-720-1379	Sequence 1379, Ap
	12	39.4	96.1	2165	11	US-09-883-839-9	Sequence 9, Appli
	13	39.4	96.1	2279	19	US-10-477-714-33	Sequence 33, Appl
c	14	29.8	72.7	6494	15	US-10-311-455-1366	Sequence 1366, Ap
	15	25.6	62.4	1388	14	US-10-185-083-26	Sequence 26, Appl
	16	25.6	62.4	1464	14	US-10-185-083-25	Sequence 25, Appl
	17	23	56.1	6494	15	US-10-311-455-1365	Sequence 1365, Ap
c	18	22.6	55.1	65140	18	US-10-203-295-1	Sequence 1, Appli
c	19	22.6	55.1	125401	18	US-10-203-295-35	Sequence 35, Appl
	20	22	53.7	468	10	US-09-918-995-24385	Sequence 24385, A
c	21	22	53.7	567	9	US-09-815-343-82	Sequence 82, Appl
c	22	22	53.7	567	17	US-10-097-105-82	Sequence 82, Appl
	23	22	53.7	4826	18	US-10-723-860-1665	Sequence 1665, Ap
	24	22	53.7	5977	19	US-10-887-553A-310	Sequence 310, App
	25	22	53.7	6036	18	US-10-723-860-6059	Sequence 6059, Ap
	26	21.8	53.2	966	17	US-10-282-122A-33315	Sequence 33315, A
	27	21.6	52.7	1408	10	US-09-933-767-31	Sequence 31, Appl
	28	21.6	52.7	1408	14	US-10-004-860-31	Sequence 31, Appl
	29	21.6	52.7	1408	14	US-10-023-282-31	Sequence 31, Appl
	30	21.2	51.7	622	17	US-10-282-596-159	Sequence 159, App
	31	21.2	51.7	630	13	US-10-027-632-18184	Sequence 18184, A
	32	21.2	51.7	630	13	US-10-027-632-18185	Sequence 18185, A
	33	21.2	51.7	630	13	US-10-027-632-18186	Sequence 18186, A
	34	21.2	51.7	630	17	US-10-027-632-18184	Sequence 18184, A
	35	21.2	51.7	630	17	US-10-027-632-18185	Sequence 18185, A
	36	21.2	51.7	630	17	US-10-027-632-18186	Sequence 18186, A
	37	21.2	51.7	1000	17	US-10-170-097-631	Sequence 631, App
	38	21.2	51.7	1000	19	US-10-926-684-631	Sequence 631, App
	39	21.2	51.7	2343	17	US-10-170-097-652	Sequence 652, App
	40	21.2	51.7	2343	19	US-10-926-684-652	Sequence 652, App
	41	21.2	51.7	2348	17	US-10-240-425-1325	Sequence 1325, Ap
	42	21.2	51.7	2368	18	US-10-741-601-232	Sequence 232, App
	43	21.2	51.7	2368	19	US-10-741-600-671	Sequence 671, App
	44	21.2	51.7	2867	18	US-10-741-601-233	Sequence 233, App
	45	21.2	51.7	2867	19	US-10-741-600-672	Sequence 672, App

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OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:08:06 ; Search time 2468.2 Seconds
(without alignments)
632.297 Million cell updates/sec

Title: US-09-883-839-1-A174_COPY_154_194
Perfect score: 41
Sequence: 1 gaaaagtctcgggtgctcctg.....ctacctgcacagcggtgcc 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	%		DB	ID	Description
			Query	Match Length			
	1	39.4	96.1	582	5	BP346782	BP346782 BP346782
	2	38.4	93.7	750	7	CO934661	CO934661 AGENCOURT
	3	37.8	92.2	718	7	CO928559	CO928559 AGENCOURT
c	4	30.4	74.1	520	8	B82759	B82759 RPCI11-17K2
	5	24.4	59.5	601	9	BX223425	BX223425 Danio rer
	6	24.4	59.5	625	9	BX211549	BX211549 Danio rer
c	7	24.2	59.0	845	4	BI218680	BI218680 602938120
c	8	23.6	57.6	603	2	AW607677	AW607677 MR3-HT048
c	9	23.4	57.1	542	4	BI994041	BI994041 1031006E1

c	10	23.4	57.1	670	4	BI717036	BI717036	1031016A0
	11	23.4	57.1	768	9	CG824720	CG824720	SOYAX34TV
	12	23.4	57.1	889	2	BE868446	BE868446	601444440
c	13	23	56.1	688	7	CF842061	CF842061	psHB017xJ
c	14	23	56.1	690	7	CF842110	CF842110	psHB017xO
	15	22.4	54.6	886	8	BZ669338	BZ669338	PUBHM52TD
c	16	22	53.7	252	2	BE159402	BE159402	MR0-HT040
c	17	22	53.7	254	2	BF825923	BF825923	CM4-HN002
c	18	22	53.7	263	2	BE092628	BE092628	CM1-BT073
	19	22	53.7	396	7	CO336884	CO336884	EN13425.5
c	20	22	53.7	399	2	BE159692	BE159692	MR0-HT040
c	21	22	53.7	403	1	AI248209	AI248209	qh70a05.x
	22	22	53.7	408	2	AW619104	AW619104	432 MARC
	23	22	53.7	438	2	AW619103	AW619103	431 MARC
	24	22	53.7	456	1	AI531817	AI531817	SD03086.5
c	25	22	53.7	460	7	CF157031	CF157031	B0643H02-
c	26	22	53.7	461	7	CF161394	CF161394	B0697A09-
	27	22	53.7	480	1	AA307826	AA307826	EST178681
	28	22	53.7	482	2	BF499309	BF499309	AT13840.5
	29	22	53.7	492	6	CB108500	CB108500	K-EST0148
	30	22	53.7	501	5	BX496401	BX496401	DKFZp779H
	31	22	53.7	503	1	AI532414	AI532414	SD03926.5
	32	22	53.7	511	1	AA826632	AA826632	of05g02.s
	33	22	53.7	513	4	BG107496	BG107496	602277615
	34	22	53.7	527	1	AI543545	AI543545	SD10338.5
	35	22	53.7	538	4	BM829204	BM829204	K-EST0102
	36	22	53.7	541	1	AA308702	AA308702	EST179513
	37	22	53.7	546	1	AI533846	AI533846	SD05816.5
	38	22	53.7	563	6	CB110915	CB110915	K-EST0152
	39	22	53.7	563	6	CB131884	CB131884	K-EST0182
	40	22	53.7	569	4	BG392107	BG392107	602410090
	41	22	53.7	570	1	AI532916	AI532916	SD04566.5
	42	22	53.7	577	5	BP268299	BP268299	BP268299
	43	22	53.7	577	7	CN352530	CN352530	170004251
	44	22	53.7	581	5	BP204840	BP204840	BP204840
	45	22	53.7	581	7	CN352538	CN352538	170005999

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OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:08:06 ; Search time 570 Seconds
(without alignments)
3485.375 Million cell updates/sec

Title: US-09-883-839-1-A124_COPY_104_144
Perfect score: 41
Sequence: 1 gcaggagctgtggcagcggc.....aaaggaagcggctgaggcgc 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	39.4	96.1	1473	9	HSU12569	U12569 Human mu op
2	39.4	96.1	1610	6	AR106017	AR106017 Sequence
3	39.4	96.1	1610	9	HUMOPIOIDA	L29301 Homo sapien

	4	39.4	96.1	2150	6	CQ725069	CQ725069 Sequence
	5	39.4	96.1	2160	6	AR162044	AR162044 Sequence
	6	39.4	96.1	2162	6	A87781	A87781 Sequence 7
	7	39.4	96.1	2162	6	AR181331	AR181331 Sequence
	8	39.4	96.1	2162	6	AR182295	AR182295 Sequence
	9	39.4	96.1	2162	6	AR270816	AR270816 Sequence
	10	39.4	96.1	2162	6	AR301230	AR301230 Sequence
	11	39.4	96.1	2162	6	AX548900	AX548900 Sequence
	12	39.4	96.1	2162	9	HUMMOR1X	L25119 Human Mu op
	13	39.4	96.1	3759	9	AF153500	AF153500 Homo sapi
	14	39.4	96.1	83889	9	AY587764	AY587764 Homo sapi
C	15	39.4	96.1	96310	9	AL136444	AL136444 Human DNA
	16	39.4	96.1	182048	2	AC027439	AC027439 Homo sapi
C	17	39.4	96.1	182383	2	AC021745	AC021745 Homo sapi
	18	32.4	79.0	163	9	AY292290	AY292290 Homo sapi
	19	32	78.0	6494	6	AX346294	AX346294 Sequence
	20	32	78.0	6494	6	AX348523	AX348523 Sequence
	21	31.4	76.6	1881	4	AF521309	AF521309 Sus scrof
	22	31.4	76.6	1881	4	PIGMUOPR	L38645 Sus scrofa
	23	27.2	66.3	307337	1	BX842656	BX842656 Bdellovib
	24	26.6	64.9	500	11	DM172F1T	AL023357 Drosophil
C	25	26.2	63.9	68903	9	HS92M18	Z73359 Human DNA s
C	26	26.2	63.9	79506	9	AL137247	AL137247 Human DNA
	27	26.2	63.9	110000	2	LMFLCHR34_07	Continuation (8 of
	28	25.6	62.4	4354	6	CQ580638	CQ580638 Sequence
C	29	25.6	62.4	6953	6	CQ580637	CQ580637 Sequence
C	30	25.6	62.4	37512	2	AL513162	AL513162 Drosophil
C	31	25.6	62.4	45672	3	DMC22E5	AL031765 Drosophil
C	32	25.6	62.4	46012	2	AL513225	AL513225 Drosophil
	33	25.6	62.4	77656	2	AC017522	AC017522 Drosophil
C	34	25.6	62.4	136465	8	AC136228	AC136228 Oryza sat
C	35	25.6	62.4	169618	3	AC105055	AC105055 Drosophil
C	36	25.6	62.4	177724	3	AC104146	AC104146 Drosophil
C	37	25.6	62.4	300933	3	AE003422	AE003422 Drosophil
	38	25.2	61.5	3192	8	AK067109	AK067109 Oryza sat
	39	25.2	61.5	3825	6	AX654161	AX654161 Sequence
C	40	25.2	61.5	115190	8	AP004153	AP004153 Oryza sat
C	41	25.2	61.5	118814	8	AP004240	AP004240 Oryza sat
	42	25.2	61.5	155154	8	AC069158	AC069158 Genomic S
	43	25.2	61.5	166509	9	AC069542	AC069542 Homo sapi
	44	25.2	61.5	188006	2	AC147422	AC147422 Oryctolag
	45	25.2	61.5	194282	2	AC068897	AC068897 Homo sapi

OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:08:06 ; Search time 280 Seconds
(without alignments)
866.819 Million cell updates/sec

Title: US-09-883-839-1-A124_COPY_104_144
Perfect score: 41
Sequence: 1 gcaggagctgtggcagcggc.....aaaggaagcggctgaggcgc 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	39.4	96.1	593	12	ACH67429	Ach67429 Human gen
	2	39.4	96.1	1431	6	ABS54812	Abs54812 cDNA enco
	3	39.4	96.1	1473	6	ABS54816	Abs54816 cDNA enco
	4	39.4	96.1	1610	2	AAQ89226	Aaq89226 Human mu
	5	39.4	96.1	1610	3	AAA59503	Aaa59503 cDNA enco
	6	39.4	96.1	1610	13	ADR44881	Adr44881 Human mu-
	7	39.4	96.1	2149	6	ABS54815	Abs54815 cDNA enco
	8	39.4	96.1	2160	2	AAQ93102	Aaq93102 Human mu
	9	39.4	96.1	2162	2	AAV61995	Aav61995 Human mu-

	10	39.4	96.1	2162	2	AAV61986	Aav61986 Human mu-
	11	39.4	96.1	2162	2	AAV61991	Aav61991 Human mu-
	12	39.4	96.1	2162	2	AAV61988	Aav61988 Human mu-
	13	39.4	96.1	2162	2	AAV61984	Aav61984 Human mu-
	14	39.4	96.1	2162	2	AAV61994	Aav61994 Human mu-
	15	39.4	96.1	2162	2	AAV61987	Aav61987 Human mu-
	16	39.4	96.1	2162	2	AAV61992	Aav61992 Human mu-
	17	39.4	96.1	2162	2	AAV61990	Aav61990 Human mu-
	18	39.4	96.1	2162	2	AAV61993	Aav61993 Human mu-
	19	39.4	96.1	2162	2	AAV61985	Aav61985 Human mu-
	20	39.4	96.1	2162	2	AAV61989	Aav61989 Human mu-
	21	39.4	96.1	2162	3	AAZ88470	Aaz88470 Human mu
	22	39.4	96.1	2162	6	ABK14953	Abk14953 Human mu
	23	39.4	96.1	2162	8	ABZ42697	Abz42697 Human opi
	24	39.4	96.1	2162	10	ADC21534	Adc21534 Human DNA
	25	39.4	96.1	2162	10	ACA56781	Aca56781 Human sig
	26	39.4	96.1	2162	12	ADI56577	Adi56577 Human pol
	27	39.4	96.1	2162	12	ADO30013	Ado30013 Human GPC
	28	39.4	96.1	2279	8	AAD51226	Aad51226 Human REM
	29	39.4	96.1	9426	13	ADR44835	Adr44835 FIV opioi
c	30	39.4	96.1	9569	13	ADR44842	Adr44842 FIV-NSE-H
	31	39.4	96.1	10472	13	ADR44876	Adr44876 Plasmid p
	32	32	78.0	6494	6	ABL33392	Abl33392 Human imm
	33	32	78.0	6494	6	AAD28390	Aad28390 Human che
	34	31.4	76.6	1881	13	ADR44850	Adr44850 Porcine m
	35	25.6	62.4	4354	4	ABL07437	Abl07437 Drosophil
c	36	25.6	62.4	6953	4	ABL07436	Abl07436 Drosophil
c	37	25.2	61.5	2967	10	ADD25636	Add25636 Binding d
	38	25.2	61.5	3825	8	ADA70708	Ada70708 Rice gene
	39	25	61.0	1791	12	ADO14235	Ado14235 Human CDK
	40	25	61.0	1827	3	AAF18251	Aaf18251 Lung canc
c	41	25	61.0	2394	12	ADO29741	Ado29741 Mouse nov
c	42	25	61.0	2397	6	AAD29587	Aad29587 Mouse gam
	43	25	61.0	3032	4	ABL07891	Abl07891 Drosophil
	44	25	61.0	5299	4	ABL07890	Abl07890 Drosophil
	45	25	61.0	7018	12	ADP74220	Adp74220 Human cyc

OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:08:06 ; Search time 82.4 Seconds
(without alignments)
814.167 Million cell updates/sec

Title: US-09-883-839-1-A124_COPY_104_144
Perfect score: 41
Sequence: 1 gcaggagctgtggcagcggc.....aaaggaagcggctgaggcgc 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
1	39.4	96.1	1610	3	US-08-889-108-7	Sequence 7, Appli
2	39.4	96.1	1610	5	PCT-US94-10358-7	Sequence 7, Appli
3	39.4	96.1	2160	3	US-08-188-275A-1	Sequence 1, Appli
4	39.4	96.1	2162	3	US-09-351-198-1	Sequence 1, Appli
5	39.4	96.1	2162	3	US-09-113-426-1	Sequence 1, Appli
6	39.4	96.1	2162	4	US-09-016-434-1379	Sequence 1379, Ap
7	39.4	96.1	2162	4	US-09-355-709C-7	Sequence 7, Appli
c 8	25.2	61.5	75176	4	US-09-949-016-13300	Sequence 13300, A
9	25	61.0	422	4	US-09-270-767-5717	Sequence 5717, Ap
10	25	61.0	422	4	US-09-270-767-20999	Sequence 20999, A
11	25	61.0	1459	4	US-09-949-016-5837	Sequence 5837, Ap
12	25	61.0	7736	4	US-09-949-016-17579	Sequence 17579, A
c 13	23.2	56.6	1893	1	US-08-271-667B-5	Sequence 5, Appli
c 14	23.2	56.6	1893	3	US-08-765-889C-18	Sequence 18, Appl
c 15	23.2	56.6	1893	5	PCT-US95-07855-18	Sequence 18, Appl

C	16	23.2	56.6	2101	3	US-08-765-889C-5	Sequence 5, Appli
C	17	23.2	56.6	2101	5	PCT-US95-07855-5	Sequence 5, Appli
C	18	23.2	56.6	2304	1	US-08-271-667B-6	Sequence 6, Appli
C	19	23.2	56.6	2304	3	US-08-765-889C-19	Sequence 19, Appl
C	20	23.2	56.6	2304	5	PCT-US95-07855-19	Sequence 19, Appl
	21	23	56.1	952	4	US-09-023-655-1424	Sequence 1424, Ap
	22	23	56.1	2590	4	US-09-949-016-4641	Sequence 4641, Ap
	23	23	56.1	8078	3	US-09-702-251-3	Sequence 3, Appli
	24	23	56.1	21723	4	US-09-949-016-16383	Sequence 16383, A
	25	22.6	55.1	3224	3	US-08-965-729A-2	Sequence 2, Appli
C	26	22.4	54.6	1329	4	US-09-902-540-4969	Sequence 4969, Ap
	27	22.4	54.6	1524	4	US-09-949-016-5791	Sequence 5791, Ap
	28	22.4	54.6	2156	4	US-09-086-663A-78	Sequence 78, Appl
	29	22.4	54.6	4835	1	US-08-386-495-9	Sequence 9, Appli
	30	22.4	54.6	4835	5	PCT-US96-02331-9	Sequence 9, Appli
C	31	22.4	54.6	12286	4	US-09-902-540-1035	Sequence 1035, Ap
	32	22.4	54.6	128723	4	US-09-949-016-17533	Sequence 17533, A
	33	22.2	54.1	1782	4	US-09-949-016-3695	Sequence 3695, Ap
	34	22.2	54.1	1926	4	US-09-023-655-312	Sequence 312, App
	35	22.2	54.1	8983	4	US-09-949-016-15437	Sequence 15437, A
C	36	22	53.7	362	4	US-09-702-705-1167	Sequence 1167, Ap
C	37	22	53.7	362	4	US-09-736-457-1167	Sequence 1167, Ap
C	38	22	53.7	362	4	US-09-614-124B-1167	Sequence 1167, Ap
C	39	22	53.7	362	4	US-09-671-325-1167	Sequence 1167, Ap
C	40	22	53.7	362	4	US-09-658-824-1167	Sequence 1167, Ap
	41	22	53.7	19377	4	US-09-949-016-15198	Sequence 15198, A
C	42	22	53.7	40261	4	US-09-949-016-11773	Sequence 11773, A
C	43	22	53.7	40265	4	US-09-949-016-16168	Sequence 16168, A
	44	21.8	53.2	530	4	US-09-640-211A-62	Sequence 62, Appl
C	45	21.8	53.2	573	4	US-09-252-991A-12649	Sequence 12649, A

OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:41:31 ; Search time 353 Seconds
(without alignments)
710.847 Million cell updates/sec

Title: US-09-883-839-1-A124_COPY_104_144
Perfect score: 41
Sequence: 1 gcaggagctgtggcagcggc.....aaaggaagcggctgaggcgc 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5662332 seqs, 3060109652 residues

Total number of hits satisfying chosen parameters: 11324664

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID		Description

c	1	39.4	96.1	593	16	US-10-029-386-624	Sequence 624, App
	2	39.4	96.1	1431	14	US-10-080-917-6	Sequence 6, Appli
	3	39.4	96.1	1473	14	US-10-080-917-13	Sequence 13, Appl
	4	39.4	96.1	2149	14	US-10-080-917-12	Sequence 12, Appl
	5	39.4	96.1	2162	11	US-09-883-839-1	Sequence 1, Appli
	6	39.4	96.1	2162	11	US-09-883-839-3	Sequence 3, Appli
	7	39.4	96.1	2162	11	US-09-883-839-5	Sequence 5, Appli
	8	39.4	96.1	2162	11	US-09-883-839-7	Sequence 7, Appli
	9	39.4	96.1	2162	11	US-09-883-839-8	Sequence 8, Appli
	10	39.4	96.1	2162	15	US-10-225-567A-185	Sequence 185, App
	11	39.4	96.1	2162	17	US-10-305-720-1379	Sequence 1379, Ap
	12	39.4	96.1	2165	11	US-09-883-839-9	Sequence 9, Appli
	13	39.4	96.1	2279	19	US-10-477-714-33	Sequence 33, Appl
	14	32	78.0	6494	15	US-10-311-455-1365	Sequence 1365, Ap
c	15	25.2	61.5	169	18	US-10-719-993-2927	Sequence 2927, Ap
c	16	25.2	61.5	169	18	US-10-719-993-2934	Sequence 2934, Ap
c	17	25.2	61.5	201	18	US-10-719-993-2931	Sequence 2931, Ap
c	18	25.2	61.5	201	18	US-10-719-993-2936	Sequence 2936, Ap
c	19	25.2	61.5	201	18	US-10-719-993-25179	Sequence 25179, A
c	20	25.2	61.5	201	18	US-10-719-993-25255	Sequence 25255, A
c	21	25.2	61.5	2490	18	US-10-719-993-182	Sequence 182, App
c	22	25.2	61.5	2967	15	US-10-207-655-197	Sequence 197, App
c	23	25.2	61.5	2967	18	US-10-719-993-181	Sequence 181, App
c	24	25.2	61.5	2967	19	US-10-887-553A-573	Sequence 573, App
	25	25.2	61.5	4165	18	US-10-437-963-69419	Sequence 69419, A
c	26	25.2	61.5	83784	18	US-10-719-993-6818	Sequence 6818, Ap
	27	25	61.0	426	18	US-10-425-115-39415	Sequence 39415, A
	28	25	61.0	1269	9	US-09-771-161A-21	Sequence 21, Appl
	29	25	61.0	1791	18	US-10-635-854A-2	Sequence 2, Appli
	30	25	61.0	1827	9	US-09-925-302-270	Sequence 270, App
	31	25	61.0	1827	10	US-09-925-302-270	Sequence 270, App
	32	25	61.0	7018	18	US-10-315-765-4	Sequence 4, Appli
c	33	25	61.0	60367	18	US-10-322-281-372	Sequence 372, App
	34	24.8	60.5	2530	18	US-10-425-115-5126	Sequence 5126, Ap
	35	24.6	60.0	105	15	US-10-106-698-3234	Sequence 3234, Ap
c	36	24.2	59.0	856	17	US-10-424-599-138239	Sequence 138239,
c	37	24	58.5	1217	18	US-10-739-930-4134	Sequence 4134, Ap
	38	23.6	57.6	3715	17	US-10-443-108-1	Sequence 1, Appli
	39	23.4	57.1	555	11	US-09-876-143-686	Sequence 686, App
	40	23.4	57.1	1023	18	US-10-437-963-29809	Sequence 29809, A
	41	23.4	57.1	1660	18	US-10-437-963-37505	Sequence 37505, A
	42	23.4	57.1	6471	17	US-10-172-118-1516	Sequence 1516, Ap
	43	23.4	57.1	6471	17	US-10-342-887-1516	Sequence 1516, Ap
	44	23.4	57.1	7494	16	US-10-161-051-190	Sequence 190, App
c	45	23.2	56.6	294	17	US-10-428-681-102	Sequence 102, App

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:08:06 ; Search time 2468.2 Seconds
(without alignments)
632.297 Million cell updates/sec

Title: US-09-883-839-1-A124_COPY_104_144
Perfect score: 41
Sequence: 1 gcaggagctgtggcagcggc.....aaaggaagcggctgaggcgc 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Match	Query Length	DB ID	Description
	1	39.4	96.1	582	5	BP346782 BP346782
	2	26.2	63.9	509	8	AZ564209 RPCI-23-2
c	3	25.8	62.9	670	8	BZ068291 ljt09a03.
	4	25.6	62.4	909	1	AL516020 AL516020
c	5	25.2	61.5	581	5	BP229974 BP229974
	6	25.2	61.5	587	9	CL726186 OR_BB005
	7	25.2	61.5	600	8	BZ374031 iel8a04.g
	8	25.2	61.5	629	8	CC165364 ii90c06.g
c	9	25.2	61.5	648	9	CC696082 OGWDQ43TH

	10	25.2	61.5	682	4	BG706182	BG706182	602669460
	11	25.2	61.5	693	8	CC165363	CC165363	ii90c06.g
c	12	25.2	61.5	780	1	AU118708	AU118708	AU118708
	13	25.2	61.5	879	9	CC703094	CC703094	OGULB72TH
c	14	25.2	61.5	879	9	CC703100	CC703100	OGULB72TV
	15	25.2	61.5	3699	9	CL967776	CL967776	OsIFCC015
	16	25	61.0	268	5	BX631829	BX631829	BX631829
	17	25	61.0	358	1	AI536944	AI536944	tm87b02.x
	18	25	61.0	382	1	AI673007	AI673007	we59d03.x
	19	25	61.0	389	2	BF445599	BF445599	nae36d07.
	20	25	61.0	419	7	CO299867	CO299867	EK176761.
	21	25	61.0	423	1	AI872498	AI872498	ty42h05.x
	22	25	61.0	424	6	CA941385	CA941385	ir34e05.x
	23	25	61.0	458	1	AI818842	AI818842	wk92a05.x
	24	25	61.0	472	2	BF514175	BF514175	UI-H-BW1-
	25	25	61.0	488	1	AI932218	AI932218	wp65g03.x
	26	25	61.0	505	2	BF488501	BF488501	AT23790.5
	27	25	61.0	572	2	AW166372	AW166372	xn52b08.x
	28	25	61.0	587	2	AW072062	AW072062	wy84a01.x
	29	25	61.0	598	5	BP220035	BP220035	BP220035
	30	25	61.0	601	2	BE740329	BE740329	601594611
	31	25	61.0	602	1	AI222414	AI222414	qh04e08.x
c	32	25	61.0	627	6	CA751220	CA751220	UI-M-FD0-
	33	25	61.0	628	4	BG180057	BG180057	602329624
c	34	25	61.0	636	7	CK773957	CK773957	962653 MA
	35	25	61.0	667	2	AW025909	AW025909	wv71f05.x
	36	25	61.0	671	4	BG702709	BG702709	602684255
	37	25	61.0	701	2	AW025900	AW025900	wv71e05.x
	38	25	61.0	706	4	BI836452	BI836452	603082823
	39	25	61.0	707	2	BE550494	BE550494	7a27d06.x
c	40	25	61.0	707	6	CB247342	CB247342	UI-M-FI0-
	41	25	61.0	720	7	CF994752	CF994752	AGENCOURT
	42	25	61.0	800	2	BF528677	BF528677	602043426
	43	25	61.0	854	9	CNS078J8	AL434058	T7 end of
	44	25	61.0	855	4	BI256406	BI256406	602974423
	45	25	61.0	865	5	BQ436563	BQ436563	AGENCOURT

Title: US-09-883-839-1-T153_COPY_133_173
 Perfect score: 41
 Sequence: 1 cggctgaggcgcttggaacc.....gaaaagtctcgggtgctcctg 41

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : GenEmbl:*
 1: gb_ba:*
 2: gb_htg:*
 3: gb_in:*
 4: gb_om:*
 5: gb_ov:*
 6: gb_pat:*
 7: gb_ph:*
 8: gb_pl:*
 9: gb_pr:*
 10: gb_ro:*
 11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	39.4	96.1	158	9 AY292291	AY292291 Homo sapi
2	39.4	96.1	163	9 AY292290	AY292290 Homo sapi
3	39.4	96.1	1473	9 HSU12569	U12569 Human mu op
4	39.4	96.1	1610	6 AR106017	AR106017 Sequence
5	39.4	96.1	1610	9 HUMOPIOIDA	L29301 Homo sapien
6	39.4	96.1	2150	6 CQ725069	CQ725069 Sequence
7	39.4	96.1	2160	6 AR162044	AR162044 Sequence
8	39.4	96.1	2162	6 A87781	A87781 Sequence 7
9	39.4	96.1	2162	6 AR181331	AR181331 Sequence
10	39.4	96.1	2162	6 AR182295	AR182295 Sequence
11	39.4	96.1	2162	6 AR270816	AR270816 Sequence
12	39.4	96.1	2162	6 AR301230	AR301230 Sequence
13	39.4	96.1	2162	6 AX548900	AX548900 Sequence
14	39.4	96.1	2162	9 HUMMOR1X	L25119 Human Mu op

	15	39.4	96.1	3759	9	AF153500	AF153500 Homo sapi
	16	39.4	96.1	83889	9	AY587764	AY587764 Homo sapi
c	17	39.4	96.1	96310	9	AL136444	AL136444 Human DNA
	18	39.4	96.1	182048	2	AC027439	AC027439 Homo sapi.
c	19	39.4	96.1	182383	2	AC021745	AC021745 Homo sapi
	20	30	73.2	1710	10	AY166606	AY166606 Cavia por
	21	29.4	71.7	1468	9	AY364230	AY364230 Homo sapi
	22	29	70.7	1401	10	RATMOPIOID	L22455 Rat mu opio
	23	29	70.7	1448	10	RNU02083	U02083 Rattus norv
	24	29	70.7	1586	10	RATMORA	L13069 Rattus norv
	25	29	70.7	1618	6	AR106013	AR106013 Sequence
	26	29	70.7	1618	6	AR106014	AR106014 Sequence
	27	29	70.7	1618	6	AR153354	AR153354 Sequence
	28	29	70.7	1618	6	AR153355	AR153355 Sequence
	29	29	70.7	1944	10	S79903	S79903 mu opioid r
	30	29	70.7	2397	10	RATRORB	D16349 Rattus norv
c	31	29	70.7	227058	2	AC115492	AC115492 Rattus no
	32	29	70.7	234399	2	AC117147	AC117147 Rattus no
	33	28.4	69.3	1881	4	AF521309	AF521309 Sus scrof
	34	28.4	69.3	1881	4	PIGMUOPR	L38645 Sus scrofa
c	35	27	65.9	108845	6	CQ869594	CQ869594 Sequence
	36	27	65.9	186854	2	AC110185	AC110185 Mus muscu
	37	27	65.9	202308	10	AC139039	AC139039 Mus muscu
	38	26.6	64.9	6494	6	AX346294	AX346294 Sequence
	39	26.6	64.9	6494	6	AX348523	AX348523 Sequence
	40	24.4	59.5	1399	9	AY038989	AY038989 Macaca fa
c	41	24	58.5	6494	6	AX346295	AX346295 Sequence
c	42	24	58.5	6494	6	AX348524	AX348524 Sequence
	43	23.6	57.6	1415	4	BTU89677	U89677 Bos taurus
	44	23.2	56.6	238123	10	AC102575	AC102575 Mus muscu
c	45	23	56.1	40560	3	CEY37H2A	AL132863 Caenorhab

Run on: May 14, 2005, 05:08:06 ; Search time 280 Seconds
 (without alignments)
 866.819 Million cell updates/sec

Title: US-09-883-839-1-T153_COPY_133_173
 Perfect score: 41
 Sequence: 1 cggctgagggcgcttggaacc.....gaaaagtctcggtgctcctg 41

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				ID	Description
	No.	Score	Match	Length	DB	Query		
c	1	39.4	96.1	593	12	ACH67429		Ach67429 Human gen
	2	39.4	96.1	1431	6	ABS54812		Abs54812 cDNA enco
	3	39.4	96.1	1473	6	ABS54816		Abs54816 cDNA enco
	4	39.4	96.1	1610	2	AAQ89226		Aaq89226 Human mu
	5	39.4	96.1	1610	3	AAA59503		Aaa59503 cDNA enco
	6	39.4	96.1	1610	13	ADR44881		Adr44881 Human mu-
	7	39.4	96.1	2149	6	ABS54815		Abs54815 cDNA enco
	8	39.4	96.1	2160	2	AAQ93102		Aaq93102 Human mu
	9	39.4	96.1	2162	2	AAV61995		Aav61995 Human mu-
	10	39.4	96.1	2162	2	AAV61986		Aav61986 Human mu-
	11	39.4	96.1	2162	2	AAV61991		Aav61991 Human mu-

12	39.4	96.1	2162	2	AAV61988	Aav61988 Human mu-
13	39.4	96.1	2162	2	AAV61984	Aav61984 Human mu-
14	39.4	96.1	2162	2	AAV61994	Aav61994 Human mu-
15	39.4	96.1	2162	2	AAV61987	Aav61987 Human mu-
16	39.4	96.1	2162	2	AAV61992	Aav61992 Human mu-
17	39.4	96.1	2162	2	AAV61990	Aav61990 Human mu-
18	39.4	96.1	2162	2	AAV61993	Aav61993 Human mu-
19	39.4	96.1	2162	2	AAV61985	Aav61985 Human mu-
20	39.4	96.1	2162	2	AAV61989	Aav61989 Human mu-
21	39.4	96.1	2162	3	AAZ88470	Aaz88470 Human mu
22	39.4	96.1	2162	6	ABK14953	Abk14953 Human mu
23	39.4	96.1	2162	8	ABZ42697	Abz42697 Human opi
24	39.4	96.1	2162	10	ADC21534	Adc21534 Human DNA
25	39.4	96.1	2162	10	ACA56781	Aca56781 Human sig
26	39.4	96.1	2162	12	ADI56577	Adi56577 Human pol
27	39.4	96.1	2162	12	ADO30013	Ado30013 Human GPC
28	39.4	96.1	2279	8	AAD51226	Aad51226 Human REM
29	39.4	96.1	9426	13	ADR44835	Adr44835 FIV opioi
C 30	39.4	96.1	9569	13	ADR44842	Adr44842 FIV-NSE-H
31	39.4	96.1	10472	13	ADR44876	Adr44876 Plasmid p
32	29	70.7	1401	13	ADR44848	Adr44848 Rat mu-op
33	29	70.7	1618	2	AAQ89222	Aaq89222 Rat mu op
34	29	70.7	1618	2	AAQ89223	Aaq89223 Transcrip
35	29	70.7	1618	3	AAA59499	Aaa59499 cDNA enco
36	28.4	69.3	1881	13	ADR44850	Adr44850 Porcine m
C 37	27	65.9	108845	13	ABD32542	Abd32542 Mouse can
38	26.6	64.9	6494	6	ABL33392	Abl33392 Human imm
39	26.6	64.9	6494	6	AAD28390	Aad28390 Human che
C 40	24	58.5	6494	6	ABL33393	Abl33393 Human imm
C 41	24	58.5	6494	6	AAD28391	Aad28391 Human che
42	23.6	57.6	1415	13	ADR44844	Adr44844 Bovine mu
43	22.6	55.1	1959	4	AAI12869	Aai12869 Probe #28
44	22.6	55.1	1959	4	ABA54570	Aba54570 Human foe
45	22.6	55.1	1959	4	AAI34225	Aai34225 Probe #29

Run on: May 14, 2005, 05:08:06 ; Search time 82.4 Seconds
 (without alignments)
 814.167 Million cell updates/sec

Title: US-09-883-839-1-T153_COPY_133_173
 Perfect score: 41
 Sequence: 1 cggctgaggcgcttggaacc.....gaaaagtctcggtgctcctg 41

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:*
 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	39.4	96.1	1610	3	US-08-889-108-7
2	39.4	96.1	1610	5	PCT-US94-10358-7
3	39.4	96.1	2160	3	US-08-188-275A-1
4	39.4	96.1	2162	3	US-09-351-198-1
5	39.4	96.1	2162	3	US-09-113-426-1
6	39.4	96.1	2162	4	US-09-016-434-1379
7	39.4	96.1	2162	4	US-09-355-709C-7
8	29	70.7	1618	3	US-08-889-108-1
9	29	70.7	1618	3	US-08-889-108-3
10	29	70.7	1618	3	US-08-120-601B-1
11	29	70.7	1618	3	US-08-120-601B-3
12	29	70.7	1618	5	PCT-US94-10358-1
13	29	70.7	1618	5	PCT-US94-10358-3
14	21.4	52.2	1610	4	US-09-761-962A-16
15	21.4	52.2	1981	3	US-08-387-707-15
16	21.4	52.2	1981	3	US-08-405-271A-15
17	21.4	52.2	2229	4	US-09-214-904-1
c 18	21.2	51.7	2020	4	US-09-567-003C-17

c	19	20.8	50.7	4797	4	US-09-976-594-988	Sequence 988, App
c	20	20.8	50.7	8600	3	US-09-457-708-1	Sequence 1, Appli
c	21	20.8	50.7	8600	4	US-09-950-046A-1	Sequence 1, Appli
c	22	20.6	50.2	601	4	US-09-949-016-73721	Sequence 73721, A
c	23	20.6	50.2	601	4	US-09-949-016-154904	Sequence 154904,
	24	20.6	50.2	1911	4	US-09-949-016-2378	Sequence 2378, Ap
	25	20.6	50.2	3114	4	US-09-620-312D-50	Sequence 50, Appl
c	26	20.6	50.2	25194	4	US-09-949-016-13887	Sequence 13887, A
	27	20.6	50.2	125192	4	US-09-949-016-14120	Sequence 14120, A
	28	20.6	50.2	340380	4	US-09-949-016-14179	Sequence 14179, A
c	29	20.6	50.2	385136	4	US-09-949-016-16073	Sequence 16073, A
	30	20.4	49.8	2002	4	US-09-016-434-1172	Sequence 1172, Ap
	31	20.4	49.8	2140	1	US-08-334-698-1	Sequence 1, Appli
	32	20.4	49.8	2140	1	US-08-228-932-1	Sequence 1, Appli
	33	20.4	49.8	2140	1	US-08-468-939-1	Sequence 1, Appli
	34	20.4	49.8	2140	2	US-08-406-855A-1	Sequence 1, Appli
	35	20.4	49.8	2140	2	US-08-722-190-1	Sequence 1, Appli
	36	20.4	49.8	2140	3	US-08-244-354-1	Sequence 1, Appli
	37	20.4	49.8	2140	3	US-09-206-899-1	Sequence 1, Appli
	38	20.4	49.8	2140	3	US-09-444-783-1	Sequence 1, Appli
	39	20.4	49.8	2140	3	US-09-688-415-1	Sequence 1, Appli
	40	20.4	49.8	2140	4	US-09-444-783-1	Sequence 1, Appli
	41	20.4	49.8	2140	5	PCT-US95-04203-1	Sequence 1, Appli
	42	20.4	49.8	33155	4	US-09-949-016-16421	Sequence 16421, A
c	43	20.4	49.8	203475	4	US-09-949-016-14516	Sequence 14516, A
c	44	20.4	49.8	203475	4	US-09-949-016-14517	Sequence 14517, A
c	45	20.4	49.8	203475	4	US-09-949-016-14518	Sequence 14518, A

OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:41:31 ; Search time 353 Seconds
(without alignments)
710.847 Million cell updates/sec

Title: US-09-883-839-1-T153_COPY_133_173
Perfect score: 41
Sequence: 1 cggctgaggcgcttggaacc.....gaaaagtctcggtgctcctg 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5662332 seqs, 3060109652 residues

Total number of hits satisfying chosen parameters: 11324664

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	%		DB	ID	Description
			Query	Match Length			
c	1	39.4	96.1	593	16	US-10-029-386-624	Sequence 624, App
	2	39.4	96.1	1431	14	US-10-080-917-6	Sequence 6, Appli
	3	39.4	96.1	1473	14	US-10-080-917-13	Sequence 13, Appl
	4	39.4	96.1	2149	14	US-10-080-917-12	Sequence 12, Appl
	5	39.4	96.1	2162	11	US-09-883-839-1	Sequence 1, Appli
	6	39.4	96.1	2162	11	US-09-883-839-3	Sequence 3, Appli
	7	39.4	96.1	2162	11	US-09-883-839-5	Sequence 5, Appli
	8	39.4	96.1	2162	11	US-09-883-839-7	Sequence 7, Appli
	9	39.4	96.1	2162	11	US-09-883-839-8	Sequence 8, Appli
	10	39.4	96.1	2162	15	US-10-225-567A-185	Sequence 185, App
	11	39.4	96.1	2162	17	US-10-305-720-1379	Sequence 1379, Ap
	12	39.4	96.1	2165	11	US-09-883-839-9	Sequence 9, Appli
	13	39.4	96.1	2279	19	US-10-477-714-33	Sequence 33, Appl
	14	29	70.7	1618	10	US-09-841-720-1	Sequence 1, Appli
	15	29	70.7	1618	10	US-09-841-720-3	Sequence 3, Appli
c	16	27	65.9	108845	18	US-10-367-094-7	Sequence 7, Appli
	17	26.6	64.9	6494	15	US-10-311-455-1365	Sequence 1365, Ap
c	18	24	58.5	6494	15	US-10-311-455-1366	Sequence 1366, Ap
	19	22.6	55.1	1959	9	US-09-864-761-2819	Sequence 2819, Ap
	20	21.8	53.2	812	18	US-10-425-115-81934	Sequence 81934, A
c	21	21.8	53.2	198161	18	US-10-775-169-52	Sequence 52, Appl
c	22	21.8	53.2	198161	18	US-10-723-860-165	Sequence 165, App
	23	21.6	52.7	1082	17	US-10-425-114-19334	Sequence 19334, A
	24	21.6	52.7	1511	17	US-10-424-599-51899	Sequence 51899, A
c	25	21.4	52.2	270	17	US-10-242-535A-3275	Sequence 3275, Ap
c	26	21.4	52.2	270	17	US-10-085-783A-3275	Sequence 3275, Ap
	27	21.4	52.2	334	14	US-10-185-083-44	Sequence 44, Appl
	28	21.4	52.2	1440	14	US-10-185-083-15	Sequence 15, Appl
	29	21.4	52.2	1569	14	US-10-185-083-17	Sequence 17, Appl
	30	21.4	52.2	1610	9	US-09-761-962-16	Sequence 16, Appl
	31	21.4	52.2	1610	15	US-10-283-300-16	Sequence 16, Appl
	32	21.4	52.2	1614	14	US-10-185-083-16	Sequence 16, Appl
	33	21.4	52.2	1981	9	US-09-823-114-15	Sequence 15, Appl
	34	21.4	52.2	1981	15	US-10-290-748-15	Sequence 15, Appl
	35	21.4	52.2	2229	9	US-09-214-904-1	Sequence 1, Appli
c	36	21.4	52.2	68255	13	US-10-087-192-772	Sequence 772, App
	37	21.4	52.2	439892	13	US-10-087-192-454	Sequence 454, App
c	38	21.2	51.7	2020	18	US-10-626-671-17	Sequence 17, Appl
	39	21	51.2	474	18	US-10-437-963-59290	Sequence 59290, A
c	40	21	51.2	1023	17	US-10-374-780A-1745	Sequence 1745, Ap
c	41	21	51.2	1340	17	US-10-424-599-60303	Sequence 60303, A
	42	21	51.2	1660	18	US-10-437-963-59286	Sequence 59286, A
c	43	20.8	50.7	201	18	US-10-719-993-5415	Sequence 5415, Ap
c	44	20.8	50.7	201	18	US-10-719-993-5421	Sequence 5421, Ap
c	45	20.8	50.7	201	18	US-10-719-993-5458	Sequence 5458, Ap

OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:08:06 ; Search time 2468.2 Seconds
(without alignments)
632.297 Million cell updates/sec

Title: US-09-883-839-1-T153_COPY_133_173
Perfect score: 41
Sequence: 1 cggctgagggcgcttggaacc.....gaaaagtctcggtgctcctg 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	39.4	96.1	582	5	BP346782	BP346782 BP346782
c	2	27.2	66.3	331	9	CL525231	CL525231 AM0652 Sa
	3	24.4	59.5	871	4	BI461844	BI461844 603207556
	4	23.8	58.0	473	8	BZ921550	BZ921550 CH240_119
	5	23.6	57.6	1060	8	CC265603	CC265603 CH261-28G
c	6	23	56.1	360	1	AV189670	AV189670 AV189670
c	7	23	56.1	360	7	D73743	D73743 CELK062FZF
	8	23	56.1	717	9	CC558335	CC558335 CH240_466
c	9	23	56.1	1212	9	AG430659	AG430659 Mus muscu
c	10	22.8	55.6	925	7	CF577636	CF577636 AGENCOURT
c	11	22.6	55.1	1037	5	BX386325	BX386325 BX386325
c	12	22.4	54.6	409	8	BH881925	BH881925 hv29a03.b
	13	22.4	54.6	724	4	BM048033	BM048033 603620353

	14	22.4	54.6	727	4	BM010950	BM010950	603634594
	15	22.4	54.6	803	8	AZ839281	AZ839281	2M0135P15
c	16	22.2	54.1	619	8	AQ554001	AQ554001	RPCI-11-4
c	17	22.2	54.1	696	8	BZ025167	BZ025167	oeh63g04.
c	18	22.2	54.1	939	9	CNS02C0P	AL190546	Tetraodon
	19	22.2	54.1	986	5	BQ707941	BQ707941	AGENCOURT
c	20	22	53.7	150	8	AQ428129	AQ428129	CITBI-E1-
c	21	22	53.7	515	7	CO782708	CO782708	BL016A_A0
c	22	22	53.7	755	8	BH686756	BH686756	BOMIE59TR
c	23	22	53.7	861	4	BF982199	BF982199	602306234
	24	21.8	53.2	368	6	CA407778	CA407778	1003927 H
c	25	21.8	53.2	408	5	BP662700	BP662700	BP662700
c	26	21.8	53.2	416	2	BE939243	BE939243	RC4-TN013
c	27	21.8	53.2	483	6	CB167424	CB167424	YOV603000
c	28	21.8	53.2	511	2	AW205908	AW205908	UI-H-BI1-
c	29	21.8	53.2	518	1	AL923021	AL923021	AL923021
	30	21.8	53.2	628	4	BG683096	BG683096	602651774
c	31	21.8	53.2	746	9	CG258174	CG258174	OGWBM56TV
	32	21.8	53.2	755	4	BG706561	BG706561	602672937
c	33	21.8	53.2	831	2	BF033843	BF033843	601456222
	34	21.8	53.2	841	8	BZ672002	BZ672002	PUBDL46TD
	35	21.8	53.2	899	9	CG258165	CG258165	OGWBM56TH
c	36	21.8	53.2	908	9	CG384368	CG384368	OGWGW75TH
	37	21.8	53.2	966	9	CG384378	CG384378	OGWGW75TV
	38	21.6	52.7	316	4	BF997147	BF997147	PM0-GN018
	39	21.6	52.7	433	2	BE440370	BE440370	sp44f11.y
	40	21.6	52.7	560	4	BG511074	BG511074	sac65d11.
	41	21.6	52.7	585	5	BU762194	BU762194	sar85f03.
	42	21.6	52.7	587	5	BU084458	BU084458	sar19f07.
	43	21.6	52.7	660	8	BZ566160	BZ566160	pacs2-164
	44	21.6	52.7	738	8	AZ273253	AZ273253	RPCI-23-1
	45	21.6	52.7	778	4	BI735494	BI735494	603357596

OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:08:06 ; Search time 570 Seconds
 (without alignments)
 3485.375 Million cell updates/sec

Title: US-09-883-839-1-GGC_COPY_167_207
 Perfect score: 41
 Sequence: 1 gctcctggctacctgcaca.....ggccggtgcccgccgcccgcg 41

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : GenEmbl:*
 1: gb_ba:*
 2: gb_htg:*
 3: gb_in:*
 4: gb_om:*
 5: gb_ov:*
 6: gb_pat:*
 7: gb_ph:*
 8: gb_pl:*
 9: gb_pr:*
 10: gb_ro:*
 11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	26.6	64.9	50	6	CQ004363	CQ004363 Sequence
2	26.6	64.9	1388	9	AY036623	AY036623 Homo sapi
3	26.6	64.9	1464	9	AY036622	AY036622 Homo sapi
4	26.6	64.9	1610	6	AR106017	AR106017 Sequence

	5	26.6	64.9	1610	9	HUMOPIOIDA	L29301 Homo sapien
	6	25.6	62.4	630	8	AK109264	AK109264 Oryza sat
	7	25.6	62.4	1126	8	AK108277	AK108277 Oryza sat
	8	25.6	62.4	118075	8	AC118675	AC118675 Genomic s
c	9	25.6	62.4	132243	8	AC148339	AC148339 Oryza sat
	10	25.2	61.5	5689	8	AF399654	AF399654 Chlamydom
	11	25	61.0	158	9	AY292291	AY292291 Homo sapi
	12	25	61.0	163	9	AY292290	AY292290 Homo sapi
	13	25	61.0	1468	9	AY364230	AY364230 Homo sapi
	14	25	61.0	1473	9	HSU12569	U12569 Human mu op
	15	25	61.0	2150	6	CQ725069	CQ725069 Sequence
	16	25	61.0	2160	6	AR162044	AR162044 Sequence
	17	25	61.0	2162	6	A87781	A87781 Sequence 7
	18	25	61.0	2162	6	AR181331	AR181331 Sequence
	19	25	61.0	2162	6	AR182295	AR182295 Sequence
	20	25	61.0	2162	6	AR270816	AR270816 Sequence
	21	25	61.0	2162	6	AR301230	AR301230 Sequence
	22	25	61.0	2162	6	AX548900	AX548900 Sequence
	23	25	61.0	2162	9	HUMMOR1X	L25119 Human Mu op
	24	25	61.0	3759	9	AF153500	AF153500 Homo sapi
	25	25	61.0	83889	9	AY587764	AY587764 Homo sapi
c	26	25	61.0	96310	9	AL136444	AL136444 Human DNA
	27	25	61.0	182048	2	AC027439	AC027439 Homo sapi
c	28	25	61.0	182383	2	AC021745	AC021745 Homo sapi
c	29	24.6	60.0	1813	10	BC057183	BC057183 Mus muscu
	30	24.6	60.0	37337	6	CQ363730	CQ363730 Sequence
c	31	24.6	60.0	110000	2	AC073804_1	Continuation (2 of
c	32	24.6	60.0	110000	2	AC073804_2	Continuation (3 of
c	33	24.6	60.0	194602	2	AC124087	AC124087 Mus muscu
c	34	24.6	60.0	237093	2	AC126111	AC126111 Rattus no
c	35	24.6	60.0	255453	2	AC109391	AC109391 Rattus no
c	36	24.2	59.0	2002	10	BC004835	BC004835 Mus muscu
	37	24	58.5	1293	9	BC074927	BC074927 Homo sapi
	38	24	58.5	204050	1	AL646070	AL646070 Ralstonia
	39	23.6	57.6	2072	6	BD206369	BD206369 Human nuc
	40	23.6	57.6	2072	6	AR400684	AR400684 Sequence
	41	23.6	57.6	2072	6	AX013188	AX013188 Sequence
	42	23.6	57.6	2175	9	AY633624	AY633624 Homo sapi
	43	23.6	57.6	2196	9	BC002326	BC002326 Homo sapi
	44	23.6	57.6	2196	9	BC003044	BC003044 Homo sapi

OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:08:06 ; Search time 280 Seconds
 (without alignments)
 866.819 Million cell updates/sec

Title: US-09-883-839-1-GGC_COPY_167_207
 Perfect score: 41
 Sequence: 1 gctcctggctacctgcaca.....ggccggtgcccgccgcccgcg 41

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	26.6	64.9	50	4	AAL29795	Aal29795 Human SNP
2	26.6	64.9	1388	10	ADG42251	Adg42251 Mu-opioid
3	26.6	64.9	1464	10	ADG42250	Adg42250 Mu-opioid
4	26.6	64.9	1610	2	AAQ89226	Aaq89226 Human mu
5	26.6	64.9	1610	3	AAA59503	Aaa59503 cDNA enco

	6	26.6	64.9	1610	13	ADR44881	Adr44881 Human mu-
c	7	25	61.0	593	12	ACH67429	Ach67429 Human gen
	8	25	61.0	1431	6	ABS54812	Abs54812 cDNA enco
	9	25	61.0	1473	6	ABS54816	Abs54816 cDNA enco
	10	25	61.0	2149	6	ABS54815	Abs54815 cDNA enco
	11	25	61.0	2160	2	AAQ93102	Aaq93102 Human mu
	12	25	61.0	2162	2	AAV61995	Aav61995 Human mu-
	13	25	61.0	2162	2	AAV61986	Aav61986 Human mu-
	14	25	61.0	2162	2	AAV61991	Aav61991 Human mu-
	15	25	61.0	2162	2	AAV61984	Aav61984 Human mu-
	16	25	61.0	2162	2	AAV61994	Aav61994 Human mu-
	17	25	61.0	2162	2	AAV61987	Aav61987 Human mu-
	18	25	61.0	2162	2	AAV61992	Aav61992 Human mu-
	19	25	61.0	2162	2	AAV61990	Aav61990 Human mu-
	20	25	61.0	2162	2	AAV61993	Aav61993 Human mu-
	21	25	61.0	2162	2	AAV61985	Aav61985 Human mu-
	22	25	61.0	2162	2	AAV61989	Aav61989 Human mu-
	23	25	61.0	2162	3	AAZ88470	Aaz88470 Human mu
	24	25	61.0	2162	6	ABK14953	Abk14953 Human mu
	25	25	61.0	2162	8	ABZ42697	Abz42697 Human opi
	26	25	61.0	2162	10	ADC21534	Adc21534 Human DNA
	27	25	61.0	2162	10	ACA56781	Aca56781 Human sig
	28	25	61.0	2162	12	ADI56577	Adi56577 Human pol
	29	25	61.0	2162	12	ADO30013	Ado30013 Human GPC
	30	25	61.0	2279	8	AAD51226	Aad51226 Human REM
	31	25	61.0	9426	13	ADR44835	Adr44835 FIV opioi
c	32	25	61.0	9569	13	ADR44842	Adr44842 FIV-NSE-H
	33	25	61.0	10472	13	ADR44876	Adr44876 Plasmid p
	34	24.6	60.0	37337	4	AAS59518	Aas59518 Propionib
	35	24.6	60.0	37337	8	ACF64447	Acf64447 Propionib
	36	23.6	57.6	401	9	ACH47687	Ach47687 Human inf
	37	23.6	57.6	432	9	ACH30106	Ach30106 Human tes
	38	23.6	57.6	433	9	ACH30049	Ach30049 Human tes
	39	23.6	57.6	493	9	ACH38361	Ach38361 Human end
	40	23.6	57.6	2072	2	AAZ42108	Aaz42108 Human end
	41	23.6	57.6	2205	13	ADP24821	Adp24821 PRO polyp
	42	23.6	57.6	2210	4	AAI59116	Aai59116 Human pol
	43	23.6	57.6	2210	5	ADQ99339	Adq99339 DNA encod
	44	23.6	57.6	2210	9	ADB49099	Adb49099 Novel hum
	45	23.6	57.6	2243	4	AAI59115	Aai59115 Human pol

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OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:08:06 ; Search time 82.4 Seconds
(without alignments)
814.167 Million cell updates/sec

Title: US-09-883-839-1-GGC_COPY_167_207
Perfect score: 41
Sequence: 1 gctcctggctacctgcaca.....ggccggtgcccgccgcccgcg 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				
No.	Score	Query	Match	Length	DB	ID	Description
1	26.6	64.9	1610	3	US-08-889-108-7	Sequence 7, Appli	
2	26.6	64.9	1610	5	PCT-US94-10358-7	Sequence 7, Appli	
3	25	61.0	2160	3	US-08-188-275A-1	Sequence 1, Appli	
4	25	61.0	2162	3	US-09-351-198-1	Sequence 1, Appli	
5	25	61.0	2162	3	US-09-113-426-1	Sequence 1, Appli	
6	25	61.0	2162	4	US-09-016-434-1379	Sequence 1379, Ap	
7	25	61.0	2162	4	US-09-355-709C-7	Sequence 7, Appli	
8	23.6	57.6	2072	4	US-09-673-395A-128	Sequence 128, App	
9	23.6	57.6	2210	4	US-09-620-312D-1009	Sequence 1009, Ap	
10	23.6	57.6	2243	4	US-09-620-312D-1008	Sequence 1008, Ap	
11	23.6	57.6	2351	4	US-09-620-312D-1007	Sequence 1007, Ap	
c 12	22.6	55.1	3842	4	US-09-976-594-279	Sequence 279, App	

c	13	22.4	54.6	825	4	US-09-902-540-8840	Sequence 8840, Ap
c	14	22.4	54.6	9335	4	US-09-902-540-940	Sequence 940, App
	15	22	53.7	7234	4	US-09-949-016-12159	Sequence 12159, A
	16	22	53.7	7235	4	US-09-949-016-16479	Sequence 16479, A
c	17	21.8	53.2	1062	4	US-09-902-540-6968	Sequence 6968, Ap
	18	21.8	53.2	1464	4	US-09-252-991A-12547	Sequence 12547, A
c	19	21.8	53.2	1854	4	US-09-252-991A-12936	Sequence 12936, A
	20	21.8	53.2	2064	1	US-08-343-428-1	Sequence 1, Appli
c	21	21.8	53.2	2288	4	US-09-620-312D-24	Sequence 24, Appl
	22	21.8	53.2	3195	4	US-09-254-594-1	Sequence 1, Appli
	23	21.8	53.2	3611	4	US-09-976-594-1109	Sequence 1109, Ap
	24	21.8	53.2	4870	4	US-09-902-540-605	Sequence 605, App
c	25	21.8	53.2	9509	4	US-09-949-016-17454	Sequence 17454, A
c	26	21.8	53.2	27933	4	US-09-949-016-12369	Sequence 12369, A
c	27	21.8	53.2	47981	4	US-09-679-279-1	Sequence 1, Appli
	28	21.8	53.2	166698	4	US-09-949-016-16038	Sequence 16038, A
	29	21.8	53.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	30	21.8	53.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	31	21.6	52.7	1320	4	US-09-252-991A-165	Sequence 165, App
c	32	21.6	52.7	1598	1	US-08-211-682-24	Sequence 24, Appl
c	33	21.6	52.7	1686	4	US-09-252-991A-155	Sequence 155, App
	34	21.6	52.7	1803	4	US-09-252-991A-170	Sequence 170, App
	35	21.6	52.7	2610	4	US-09-252-991A-175	Sequence 175, App
c	36	21.6	52.7	10106	4	US-09-949-016-17187	Sequence 17187, A
c	37	21.6	52.7	23673	3	US-09-773-816-1	Sequence 1, Appli
c	38	21.4	52.2	601	4	US-09-949-016-65252	Sequence 65252, A
	39	21.4	52.2	870	1	US-07-916-901-3	Sequence 3, Appli
c	40	21.4	52.2	888	4	US-09-311-021-155	Sequence 155, App
c	41	21.4	52.2	920	4	US-09-620-312D-132	Sequence 132, App
	42	21.4	52.2	1134	1	US-08-087-772A-14	Sequence 14, Appl
	43	21.4	52.2	1227	1	US-07-916-901-1	Sequence 1, Appli
	44	21.4	52.2	1227	1	US-08-351-473B-7	Sequence 7, Appli
	45	21.4	52.2	1230	4	US-09-543-681A-1509	Sequence 1509, Ap

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OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:41:31 ; Search time 353 Seconds
(without alignments)
710.847 Million cell updates/sec

Title: US-09-883-839-1-GGC_COPY_167_207
Perfect score: 41
Sequence: 1 gctcctggctacctcgacaca.....ggccggtgcccgccccggccg 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5662332 seqs, 3060109652 residues

Total number of hits satisfying chosen parameters: 11324664

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		DB	ID	Description
	No.	Score	Query Match	Length			
c	1	26.6	64.9	1388	14	US-10-185-083-26	Sequence 26, Appl
	2	26.6	64.9	1464	14	US-10-185-083-25	Sequence 25, Appl
	3	25.6	62.4	1347	18	US-10-437-963-2912	Sequence 2912, Ap
	4	25	61.0	593	16	US-10-029-386-624	Sequence 624, App
	5	25	61.0	1431	14	US-10-080-917-6	Sequence 6, Appli
	6	25	61.0	1473	14	US-10-080-917-13	Sequence 13, Appl
	7	25	61.0	2149	14	US-10-080-917-12	Sequence 12, Appl
	8	25	61.0	2162	11	US-09-883-839-1	Sequence 1, Appli
	9	25	61.0	2162	11	US-09-883-839-3	Sequence 3, Appli
	10	25	61.0	2162	11	US-09-883-839-5	Sequence 5, Appli
	11	25	61.0	2162	11	US-09-883-839-7	Sequence 7, Appli
	12	25	61.0	2162	11	US-09-883-839-8	Sequence 8, Appli
	13	25	61.0	2162	15	US-10-225-567A-185	Sequence 185, App
	14	25	61.0	2162	17	US-10-305-720-1379	Sequence 1379, Ap
	15	25	61.0	2165	11	US-09-883-839-9	Sequence 9, Appli
	16	25	61.0	2279	19	US-10-477-714-33	Sequence 33, Appl
	17	23.6	57.6	401	10	US-09-918-995-34899	Sequence 34899, A
	18	23.6	57.6	432	10	US-09-918-995-17318	Sequence 17318, A
	19	23.6	57.6	433	10	US-09-918-995-17261	Sequence 17261, A
	20	23.6	57.6	493	10	US-09-918-995-25573	Sequence 25573, A
	21	23.6	57.6	2210	15	US-10-037-270-1009	Sequence 1009, Ap
	22	23.6	57.6	2210	17	US-10-117-722-1009	Sequence 1009, Ap
	23	23.6	57.6	2243	15	US-10-037-270-1008	Sequence 1008, Ap
	24	23.6	57.6	2243	17	US-10-117-722-1008	Sequence 1008, Ap
	25	23.6	57.6	2351	15	US-10-037-270-1007	Sequence 1007, Ap
	26	23.6	57.6	2351	17	US-10-117-722-1007	Sequence 1007, Ap
c	27	23.4	57.1	2311	10	US-09-814-353-19138	Sequence 19138, A
c	28	23.4	57.1	2358	18	US-10-425-115-119315	Sequence 119315,
	29	23.2	56.6	499	13	US-10-027-632-135159	Sequence 135159,
	30	23.2	56.6	499	13	US-10-027-632-135160	Sequence 135160,
	31	23.2	56.6	499	17	US-10-027-632-135159	Sequence 135159,
	32	23.2	56.6	499	17	US-10-027-632-135160	Sequence 135160,
c	33	23.2	56.6	514	16	US-10-029-386-6820	Sequence 6820, Ap
c	34	23	56.1	319	10	US-09-814-353-995	Sequence 995, App
c	35	23	56.1	319	10	US-09-814-353-7364	Sequence 7364, Ap
c	36	23	56.1	462	10	US-09-814-353-13749	Sequence 13749, A
	37	23	56.1	566	18	US-10-425-115-37618	Sequence 37618, A
c	38	23	56.1	673	9	US-09-925-297-360	Sequence 360, App
	39	23	56.1	1131	17	US-10-296-115-638	Sequence 638, App
c	40	23	56.1	2485	18	US-10-755-889-433	Sequence 433, App
c	41	23	56.1	2917	10	US-09-814-353-19631	Sequence 19631, A
	42	22.6	55.1	209	16	US-10-029-386-21247	Sequence 21247, A
	43	22.6	55.1	564	16	US-10-029-386-7547	Sequence 7547, Ap
	44	22.6	55.1	701	13	US-10-027-632-168307	Sequence 168307,
	45	22.6	55.1	701	17	US-10-027-632-168307	Sequence 168307,

OM nucleic - nucleic search, using sw model

Run on: May 14, 2005, 05:08:06 ; Search time 2468.2 Seconds
(without alignments)
632.297 Million cell updates/sec

Title: US-09-883-839-1-GGC_COPY_167_207
Perfect score: 41
Sequence: 1 gctcctggctacctcgaca.....ggccggtgcccgcggccg 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	27.2	66.3	392	5	BP456446	BP456446 BP456446
c	2	26.2	63.9	425	5	BY217894	BY217894 BY217894
c	3	25.6	62.4	377	2	BB872468	BB872468 BB872468
c	4	25.6	62.4	570	5	BP454872	BP454872 BP454872
c	5	25.6	62.4	614	5	BP146308	BP146308 BP146308
c	6	25.6	62.4	643	5	BP458009	BP458009 BP458009
c	7	25.6	62.4	669	5	BP148780	BP148780 BP148780
c	8	25.6	62.4	679	4	BI182001	BI182001 UNL-P-FN-
	9	25.6	62.4	707	6	CA172566	CA172566 SCSGSB100
c	10	25.6	62.4	727	5	BP455632	BP455632 BP455632
c	11	25.6	62.4	750	5	BP150223	BP150223 BP150223
c	12	25.6	62.4	753	5	BP144546	BP144546 BP144546
c	13	25.6	62.4	770	5	BP172448	BP172448 BP172448

C	14	25.6	62.4	799	5	BP463151	BP463151	BP463151
C	15	25.6	62.4	808	5	BP144838	BP144838	BP144838
C	16	25.6	62.4	838	5	BP172775	BP172775	BP172775
C	17	25.6	62.4	857	5	BP173433	BP173433	BP173433
	18	25.2	61.5	1006	4	BI730611	BI730611	603351013
	19	25	61.0	567	7	CN236512	CN236512	WLB111C05
	20	25	61.0	582	5	BP346782	BP346782	BP346782
	21	25	61.0	750	7	CO934661	CO934661	AGENCOURT
C	22	25	61.0	962	8	CC413347	CC413347	PUHGJ03TB
C	23	24.6	60.0	320	2	BF463597	BF463597	UI-M-CG0p
C	24	24.6	60.0	322	5	BY124764	BY124764	BY124764
C	25	24.6	60.0	322	5	BY330251	BY330251	BY330251
C	26	24.6	60.0	323	5	BY318021	BY318021	BY318021
C	27	24.6	60.0	334	6	BY785590	BY785590	BY785590
C	28	24.6	60.0	335	5	BY180497	BY180497	BY180497
C	29	24.6	60.0	338	5	BY321856	BY321856	BY321856
C	30	24.6	60.0	339	5	BY199147	BY199147	BY199147
C	31	24.6	60.0	339	5	BY205979	BY205979	BY205979
C	32	24.6	60.0	343	5	BY321773	BY321773	BY321773
C	33	24.6	60.0	345	5	BY189984	BY189984	BY189984
C	34	24.6	60.0	346	5	BY219609	BY219609	BY219609
C	35	24.6	60.0	346	5	BY232385	BY232385	BY232385
C	36	24.6	60.0	347	5	BY180490	BY180490	BY180490
C	37	24.6	60.0	349	5	BY222010	BY222010	BY222010
C	38	24.6	60.0	351	5	BY195685	BY195685	BY195685
C	39	24.6	60.0	352	5	BY338859	BY338859	BY338859
C	40	24.6	60.0	352	6	BY783355	BY783355	BY783355
C	41	24.6	60.0	353	5	BY074956	BY074956	BY074956
C	42	24.6	60.0	353	5	BY209059	BY209059	BY209059
C	43	24.6	60.0	356	2	BB842729	BB842729	BB842729
C	44	24.6	60.0	356	5	BY232230	BY232230	BY232230
C	45	24.6	60.0	357	5	BY183890	BY183890	BY183890